

SEQUENCE LISTING

<110> Fox, Brian
Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN
ZACRP13

<130> 00-96C1

<150> US 09/997,610

<151> 2001-11-29

<150> US 60/253,924

<151> 2000-11-29

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1381

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)...(1381)

<400> 1

```

g ata gtg gtc ata cct gtc tta ata acg gca gtc att gag cat gta gaa 49
  ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
    1             5             10             15

gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtg ggg cct 97
Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
      20             25             30

cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg 145
Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
      35             40             45

aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtg aag 193
Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
      50             55             60

ctc agt gga aaa ctt cct ctt cct ttc aag ccc atc atc ttc aca ggg 241
Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
      65             70             75             80

gtc ctg tac aat gcc cag agg gat tta aag gag gcc atg gga gtc ttt 289
Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
      85             90             95

gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg 337
Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
      100            105            110

cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct 385
His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
      115            120            125

aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg 433
Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp

```

130	135	140	
gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt			481
Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser			
145	150	155	160
tca gaa aat ttg cac cct gac aat gtg ata aaa aag aaa aac cca ttt			529
Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe			
	165	170	175
tct gag ggg aaa ttc aag ctg gct gca gaa att tgc ata tgt aat gag			577
Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu			
	180	185	190
gag ctg aat gtt aat cct caa gac aat ggg gaa aat atc tcc tgg aca			625
Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr			
	195	200	205
tgt cag agg tct tca cag cag tcc atc aaa tca ctg gcc tgg agg cct			673
Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro			
	210	215	220
agg aga aaa tgg ttt tgt ggg aca ggc cca ggg tcc ctg tgc tgt gtg			721
Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val			
	225	230	235
cag cct aga gac ttg gtg ccc tgt gtc cca gtt aat tca gct gtg gct			769
Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala			
	245	250	255
tca gag ggt gca agc ccc aag cct tgg cag ctt cca agt ggt gtt gag			817
Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu			
	260	265	270
cct gtg ggt gca aag aag tca aga att gag gtt tgg gaa cct cca atc			865
Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile			
	275	280	285
aga ttt cag aag ata tat gga aac ccc tgg atg ccc agg cag aag ttt			913
Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe			
	290	295	300
gct gta ggg gtg ggg tcc tca tgg aga acc tct gca agg gta gta caa			961
Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln			
	305	310	315
aag gga aat gtt ggg tgg gag ccc cca cac aga gtc ccc agt ggg gct			1009
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala			
	325	330	335
cca tct agt aga gct gtg aga aga agt cca cca tcc tcc aga ctc cag			1057
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln			
	340	345	350
aag ggt aga tcc act gac agc ttg cag cat gtg cct gaa aaa tcc aca			1105
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr			
	355	360	365
gac act cag tgc cag cct gtg aaa gca gca ggg atg gag tct gta ccc			1153
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro			
	370	375	380
tac aaa acc gta gtg gca gag ctg acc aag acc gtg gga atc tac ctc			1201
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu			

385	390	395	400	
ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat				1249
Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His				
	405	410	415	
ttt gga gct tta aga ttt gac tgc ccc act gga ttt cgg act tat atg				1297
Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met				
	420	425	430	
ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc				1345
Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala				
	435	440	445	
gta ttt acc caa tgc ctg tac ctc cat tgt atg tag				1381
Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met *				
	450	455		

<210> 2
 <211> 459
 <212> PRT
 <213> Homo sapiens

<400> 2
 Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
 1 5 10 15
 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
 20 25 30
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
 35 40 45
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
 50 55 60
 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
 65 70 75 80
 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
 85 90 95
 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
 100 105 110
 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
 115 120 125
 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp
 130 135 140
 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser
 145 150 155 160
 Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe
 165 170 175
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu
 180 185 190
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
 195 200 205
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
 210 215 220
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
 225 230 235 240
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
 245 250 255
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
 260 265 270
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
 275 280 285
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
 290 295 300
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln

```

305          310          315          320
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
          325          330          335
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
          340          345          350
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
          355          360          365
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
          370          375          380
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
385          390          395          400
Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
          405          410          415
Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
          420          425          430
Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
          435          440          445
Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met
          450          455

```

```

<210> 3
<211> 1377
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Degenerate polynucleotide encoding a polypeptide
      of SEQ ID NO:2

```

```

<221> variation
<222> (1)...(1377)
<223> Each n is independently A, T, G, or C.

```

```

<221> misc_feature
<222> (1)...(1377)
<223> n = A,T,C or G

```

```

<400> 3
athgtngtna thccngtnyt nathacngcn gtnathgarc aygtngargt ngcnggncn 60
ccngcncayc cnmgncncnc ngargargtn ggncncncng gngcncncng nytnccncar 120
tayacnggng arathwsnga ratgacnaar tgyccntgyc cngayathga rmgnwsngcn 180
ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn 240
gtnytntaya aygcncarmg ngayytnaar gargcnatgg gngtnttygc ntgymgngtn 300
ccnggnaayt aytaywsnws nttygaygtg garytncayc aytgyaargt naayathtg 360
ytnatgmgn aarcathyt ngcnaayaar gargarathw snaarcarca rwsnathcar 420
gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn 480
wsngaraayy tncayccnga yaaygttnath aaraaraara ayccnttyws ngarggnaar 540
ttyaarytng cngcngarat htgyathtgy aaygargary tnaaygtnaa yccncargay 600
aayggngara ayathwsntg gacntgycar mgnwsnwsnc arcarwsnat haarwsnytn 660
gcntggmgnc cnmgnmgnaa rtggttytgy ggnacnggnc cnggnwsnyt ntgytgygtn 720
carccnmgng ayytngtncc ntgygtncn gtnaaywsng cngtngcnws ngarggngcn 780
wsnccnaarc cntggcaryt nccnwsnggn gtngarccng tnggngcnaa raarwsnmgn 840
athgargtnat gggarcncnc nathmgntty caraaratht ayggnaaycc ntggatgccn 900
mgncaraart tygcngtngg ngtnngnwsn wsntggmgna cnwsngcnmg ngtngtncar 960
aarggnaayg tnggntggga rccncncay mgngtnccnw snggngcnc nwsnwsnmgn 1020
gcngtnmgm gnwsncncnc nwsnwsnmgn ytncaraarg gnmgnwsnac ngaywsnytn 1080
carcaygtnc cngaraarws nacngayacn cartgycarc cngtnaargc ngcnggnatg 1140
garwsngtn cngaraarws nacngayacn cartgycarc cngtnaargc ngcnggnatg 1200
ytncaytgyc aygayytnga ygtngmncay ggngtnaarm gngaycaytt yggngcnytn 1260
mgnttygayt gyccnacngg nttymgnaen tayatgggnc cngtnccnyt ntgytgyggn 1320
carttyttyc cnttyggnae ngcngtntty acncartgyy tntayytnc ytgaytg 1377

```

```

<210> 4

```

<211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Aromatic motif

<221> VARIANT
 <222> (2)...(6)
 <223> Each Xaa is any amino acid residue

<221> VARIANT
 <222> (7)...(7)
 <223> Xaa is asparagine or aspartic acid

<221> VARIANT
 <222> (8)...(11)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (12)...(12)
 <223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

<221> VARIANT
 <222> (13)...(18)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (20)...(24)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (26)...(26)
 <223> Xaa is any amino acid residue

<221> VARIANT
 <222> (28)...(31)
 <223> Each Xaa is independently any amino acid residue

<400> 4
 Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa
 20 25 30

<210> 5
 <211> 1731
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1731)

<400> 5
 atg ctg ata gag gcc tat gga ggg gac ctt gtg gcc cag ggc agc aag 48
 Met Leu Ile Glu Ala Tyr Gly Gly Asp Leu Val Ala Gln Gly Ser Lys
 1 5 10 15
 aaa tgc tgc att gga gag atg ggg tac atg cga gtg aca atg gga aga 96
 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg

20	25	30	
gtt ggt agc tgg aga gaa ctg gga aag cct tca ggc atc tgg gaa atg Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met 35 40 45			144
gct ggg gat aca gag gtg aag aag aca ggg ttt ctt cag gaa ctc act Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr 50 55 60			192
ttc cag cag gag cct ggc atc tcc tcc tct cct tct tgc tcc cgc tct Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser 65 70 75 80			240
tgc cat gtg aca cca cct gct cca cct gca tct tct gcc ata att gta Cys His Val Thr Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val 85 90 95			288
aga ttc ctg agg ccc tca cca gaa gca gat gcc agc agc atg ctt att Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile 100 105 110			336
gca cag tct gta gaa ccg ata gtg gtc ata cct gtc tta ata acg gca Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala 115 120 125			384
gtc att gag cat gta gaa gtt gct gga cct cca gca cac ccc agg ccc Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro 130 135 140			432
cca gaa gaa gtg ggg cct cct ggt gca cca ggt tta cca caa tat aca Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr 145 150 155 160			480
gga gaa ata agt gaa atg aca aaa tgc ccc tgt cct gat ata gaa agg Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg 165 170 175			528
tca gcc ttt act gtg aag ctc agt gga aaa ctt cct ctt cct ttc aag Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys 180 185 190			576
ccc atc atc ttc aca ggg gtc ctg tac aat gcc cag agg gat tta aag Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys 195 200 205			624
gag gcc atg gga gtc ttt gct tgc agg gtg cct ggg aat tac tac tcc Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser 210 215 220			672
agc ttt gat gtt gag ctg cat cat tgc aag gtg aat att tgg cta atg Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met 225 230 235 240			720
agg aag caa att ttg gct aat aag gaa gaa att tct aag cag caa agc Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser 245 250 255			768
att caa gag gtg act tgg gtg ctg tta aag gca ttc agt ttc ata agg Ile Gln Glu Val Thr Trp Val Leu Lys Ala Phe Ser Phe Ile Arg 260 265 270			816
gag gca gag cat aag agt tca gaa aat ttg cac cct gac aat gtg ata Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile			864

275	280	285	
aaa aag aaa aac cca ttt tct gag ggg aaa ttc aag ctg gct gca gaa Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu 290 295 300			912
att tgc ata tgt aat gag gag ctg aat gtt aat cct caa gac aat ggg Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly 305 310 315 320			960
gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys 325 330 335			1008
tca ctg gcc tgg agg cct agg aga aaa tgg ttt tgt ggg aca ggc cca Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro 340 345 350			1056
ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro 355 360 365			1104
gtt aat tca gct gtg gct tca gag ggt gca agc ccc aag cct tgg cag Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln 370 375 380			1152
ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu 385 390 395 400			1200
gtt tgg gaa cct cca atc aga ttt cag aag ata tat gga aac ccc tgg Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp 405 410 415			1248
atg ccc agg cag aag ttt gct gta ggg gtg ggg tcc tca tgg aga acc Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr 420 425 430			1296
tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His 435 440 445			1344
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro 450 455 460			1392
cca tcc tcc aga ctc cag aag ggt aga tcc act gac agc ttg cag cat Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His 465 470 475 480			1440
gtg cct gaa aaa tcc aca gac act cag tgc cag cct gtg aaa gca gca Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala 485 490 495			1488
ggg atg gag tct gta ccc tac aaa acc gta gtg gca gag ctg acc aag Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys 500 505 510			1536
acc gtg gga atc tac ctc ttg cat tgt cat gac ctg gac gtg aga cat Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His 515 520 525			1584
gga gtc aaa aga gat cat ttt gga gct tta aga ttt gac tgc ccc act Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr 530 535 540			1632

530	535	540	
gga ttt cgg act tat atg ggg ccc gta ccc ctt tgt ttt ggc caa ttt			1680
Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe			
545	550	555	560
ttt cca ttt gga act gcc gta ttt acc caa tgc ctg tac ctc cat tgt			1728
Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys			
	565	570	575
atg			1731
Met			

<210> 6
 <211> 577
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Leu Ile Glu Ala Tyr Gly Gly Asp Leu Val Ala Gln Gly Ser Lys
 1 5 10 15
 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg
 20 25 30
 Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met
 35 40 45
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr
 50 55 60
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser
 65 70 75 80
 Cys His Val Thr Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val
 85 90 95
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile
 100 105 110
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala
 115 120 125
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro
 130 135 140
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr
 145 150 155 160
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg
 165 170 175
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys
 180 185 190
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys
 195 200 205
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser
 210 215 220
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met
 225 230 235 240
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser
 245 250 255
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg
 260 265 270
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile
 275 280 285
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu
 290 295 300
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly
 305 310 315 320
 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys
 325 330 335
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro

[illegible]

```
<210> 7
<211> 1731
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Degenerate polynucleotide sequence of zacrp13/zhp1
      of SEQ ID NO:6
```

```
<221> misc_feature
<222> (1)...(1731)
<223> n = A,T,C or G
```

<400>	7							
atgytnathg	argcntaygg	nggn gayytn	gtngcncarg	gnwsnaaraa	rtgytgyath	60		
ggngaratgg	gntayatgm	ngtnacnatg	ggnmgngtng	gnwsntggmg	ngarytnggn	120		
aarccnwsng	gnathtgga	rattgccnggn	gayacngarg	tnaaraarac	nggntytytn	180		
cargarytna	cnttycarca	rgarcenggn	athwsnsw	sncnwsntg	ywsnmngwnsn	240		
tgycaygtna	cncncncng	nccncngcn	wsnwsngcna	thathgtnmg	nttyytngmgn	300		
ccnwsnccng	argcngaygc	nwsnwsnatg	ytnathgcnc	arwsngtnga	rccnathgtn	360		
gtnathccng	tnytnathac	ngcngtnath	gar caygtng	argtngcngg	nccnccngcn	420		
cayccnmgnc	cncncgarga	rgtnggnccn	ccnggngcnc	cnggnytncc	ncartayaacn	480		
ggngaratwh	sngaratgac	naartgyccn	tgycngcnga	thgarmgnws	ngcnttyacn	540		
gtnaarytnw	sngngaaryt	nccnytnccn	tytaarecna	thathttyac	ngngtnytn	600		
tayaaygcnc	armngnayyt	naargargcn	atggngtnt	tygcntgymg	ngtnccnggn	660		
aaytaytayw	snwsnttyga	ygtngarytn	caycaytgya	argtnaayat	htggytnatg	720		
mgnaarcara	thytngcnaa	yaargargar	athwsnaarc	arcarsnat	hcargargtn	780		
acntgggtny	tnytnaargc	nttywsntty	athmgngarg	cngarcayaa	rwsnwsngar	840		
aayyntcayc	cngayaaygt	nathaaraar	aaraayccnt	tywsgcargg	naartyaayr	900		
ytngcngcng	arathtgyat	htgyaaygar	garytnaayg	tnaayccna	rgayaayggn	960		
garaayathw	sntggacntg	ycarmgnwsn	wsncarcarw	snthaarws	nytngcntgg	1020		

mgncnmgm	gnaartggtt	ytgyggnaen	ggncenggnw	snytntgytg	ygtnccn	1080
mgngayytng	tnccntgygt	nccngtnaay	wsngcngtng	cnwsngargg	ngcnwsnccn	1140
aarcntggc	arytnccnws	nggngtngar	ccngtnggng	cnaaraarws	nmgnathgar	1200
gtntgggar	cncnathmg	nttycaraar	athtayggna	ayccntggat	gccnmgnar	1260
aarttygcng	tnggngtngg	nwsnwsntgg	mgnacnwsng	cnmgngtngt	ncaraarggn	1320
aaygtnggnt	gggarccncc	ncaymgngtn	ccnwsnggng	cncnwsnws	nmgngcngtn	1380
mgnmgwnsnc	cncnwsnws	nmgnytnar	aarggnmgw	snacngayws	nytnarcar	1440
gtncngara	arwsnacnga	yacncartgy	carcngtna	argcngcngg	natggarwsn	1500
gtncntaya	aracngtngt	ngcngarytn	acnaaracng	tnggnathta	yytnytnay	1560
tgycaygayy	tngaygtngm	ncayggngtn	aarmngayc	ayttyggngc	nytnmgntty	1620
gaytgyccna	cnggnttymg	nacntayatg	ggncngtnc	cnytntgytt	yggnartty	1680
ttyccnttyg	gnacngcngt	nttyacncar	tgyytntayy	tnaytgyat	g	1731